Listing of the Claims:

This Listing of Claims replaces all the prior versions and listings of claims.

1-40. (CANCELED)

41. (CURRENTLY AMENDED) A method of determining an alteration in a nucleic acid encoding human MSH5 gene, wherein said human MSH5 is encoded by SEQ ID No.: 1, the method comprising analyzing a nucleic acid in a biological sample for an alteration in the SEQ ID No.: 1 by comparing the nucleic acid in the biological sample to that of the sequence of SEQ ID NO:1 wherein a difference in the nucleic acid in the sample compared to SEQ ID NO: 1 represents an alteration in human MSH5 gene.

42. (PREVIOUSLY PRESENTED) The method of claim 41, wherein the biological sample is selected from blood, tissue, serum, stool, urine, sputum, cerebrospinal fluid, supernatant from cell lysate and a eukaryotic cell sample.

43. (PREVIOUSLY PRESENTED) The method of claim 41, wherein the analyzing is performed using mRNA in the biological sample.

44. (PREVIOUSLY PRESENTED) The method of claim 41, wherein the analyzing is performed using DNA in the biological sample.

45. (PREVIOUSLY PRESENTED) The method of claim 41,wherein the biological sample is from an individual affected with cancer.

46. (CURRENTLY AMENDED) The method of claim 41, wherein the biological ~~specimen if~~ sample is from an individual affected with infertility.

47. (CANCELLED)

48. (CURRENTLY AMENDED) The method of claim 41, wherein the alteration is detected using a pair of oligonucleotide primers that hybridize to ~~SEQ ID NO:1 or~~ SEQ ID NOs: 3-26 or 27-50.

49. (PREVIOUSLY PRESENTED) The method of claim 41, wherein the alteration is a functional alteration and wherein the alteration is tested for being a functional alteration by comparing the results obtained with the altered human MSH5 gene encoded by SEQ ID NO:1 or its expression product with a wild type control.

50. (NEW)The method of claim 41, wherein the analysis is performed using nucleic acid

sequencing.

51. (NEW)The method of claim 41, wherein the comparison is made by looking at a genomic sample by looking at at least one individual exon.

52. (NEW) The method of claim 41, wherein the alteration is determined using restriction fragment length polymorphism using a probe or probes that specifically bind to SEQ ID NO: 1.

53. (NEW)The method of claim 41, wherein the alteration is a deletion within SEQ ID NO: 1.

54. (NEW)The method of claim 41, wherein the alteration is a point mutation within SEQ ID NO: 1.

55. (NEW)A method of determining an alteration in a nucleic acid encoding human MSH5 comprising the steps of

(a) amplifying a nucleic acid from a biological sample with primers that specifically hybridize to SEQ ID NO:1; and

(b) comparing the amplified nucleic acid to SEQ ID NO: 1,

wherein a difference in the nucleic acid from the biological sample compared to the corresponding sequence region in SEQ ID NO: 1 is indicative of an alteration in the nucleic acid encoding human MSH5.

56. (NEW)The method of claim 55, wherein at least one pair of the primers specifically hybridize to one of the exon/intron borders of human MSH5.

57. (NEW)The method of claim 56, wherein the human MSH5 exon/intron borders are selected from SEQ ID NOs: 3-26 and 27-50.

58. (NEW) The method of claim 41, wherein the comparison is made by looking at a coding region of the SEQ ID NO: 1.

59. (NEW) The method of claim 41, wherein the comparison is made by looking at a non-coding region of the SEQ ID NO: 1.